RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/759,152**

DATE: 05/30/2001
TIME: 15:39:54

Input Set : **A:\4085-235-27 CIP.ST25.txt**
Output Set: **C:\CRF3\05302001\I759152.raw**

ENTERED

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 4 <110> APPLICANT: Palmer, Michelle A.J.
 5         Gee, Melissa
 6         Tillotson, Bonnie
 7         Chang, Xiao-Jia
 9 <120> TITLE OF INVENTION: Systems for Sensitive Detection of G-Protein Coupled
10         Receptor and Orphan Receptor Function Using Reporter
11         Enzyme Mutant Complementation
13 <130> FILE REFERENCE: 4085-235-27 CIP
15 <140> CURRENT APPLICATION NUMBER: US 09/759,152
16 <141> CURRENT FILING DATE: 2001-01-16
18 <150> PRIOR APPLICATION NUMBER: US 09/654,499
19 <151> PRIOR FILING DATE: 2000-09-01
21 <150> PRIOR APPLICATION NUMBER: US 60/180,669
22 <151> PRIOR FILING DATE: 2000-02-07
24 <160> NUMBER OF SEQ ID NOS: 9
26 <170> SOFTWARE: PatentIn version 3.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 6700
30 <212> TYPE: DNA
31 <213> ORGANISM: Unknown
33 <220> FEATURE:
34 <223> OTHER INFORMATION: pICAST ALC.
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37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1457)..(4486)
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45 tcctgccccg gctcagggcc aagaacagat ggtccccaga tgcggtccag ccctcagcag     180
47 tttctagaga accatcagat gtttccaggg tgccccaagg acctgaaatg accctgtgcc     240
49 ttatttgaac taaccaatca gttcgcttct cgcttctgtt cgcgcgcttc tgctccccga     300
51 gctcaataaa agagcccaca acccctcact cggggcgcca gtcctccgat tgactgagtc     360
53 gcccgggtac ccgtgtatcc aataaaccct cttgcagttg catccgactt gtggtctcgc     420
55 tgttccttgg gagggtctcc tctgagtgat tgactacccg tcagcggggg tctttcattt     480
57 gggggctcgt ccgggatcgg gagacccctg cccagggacc accgacccac caccgggagg     540
59 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta     600
61 tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcggacc cgtggtggaa     660
63 ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccagggac tttgggggcc     720
65 gtttttgtgg cccgacctga ggaagggagt cgatgtggaa tccgaccccg tcaggatatg     780
67 tggttctggt aggagacgag aacctaaaac agttcccgcc tccgtctgaa ttttttgcttt     840
69 cggtttggaa ccgaagccgc gcgtcttgtc tgctgcagca tcgttctgtg ttgtctctgt     900
71 ccgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt     960
73 ttgaccttag gtaactggaa agatgtcgag cggctcgctc acaaccagtc ggtagatgtc    1020
75 aagaagagac gttgggttac cttctgctct gcagaatggc caacctttaa cgtcggatgg    1080
77 ccgcgagacg gcacctttaa ccgagacctc atcacccagg ttaagatcaa ggtctttttca    1140
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 83 ccatccgccc cgtctctccc ccttgaacct cctcgttcga ccccgcctcg atcctccctt   1320
 85 tatccagccc tcactccttc tctaggcgcc ggccgctcta gcccattaat acgactcact   1380
 87 atagggcgat tcgaatcagg ccttggcgcg ccggatcctt aattaagcgc aattgggagg   1440
 89 tggcggtagc ctcgag atg ggc gtg att acg gat tca ctg gcc gtc gtg gcc   1492
 90                    Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala
 91                     1                 5                   10
 93 cgc acc gat cgc cct tcc caa cag tta cgc agc ctg aat ggc gaa tgg     1540
 94 Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp
 95      15                  20                  25
 97 cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg     1588
 98 Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu
 99      30                  35                  40
101 gag tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg     1636
102 Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp
103 45                  50                  55                  60
105 cag atg cac ggt tac gat gcg ccc atc tac acc aac gtg acc tat ccc     1684
106 Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro
107                  65                  70                  75
109 att acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt     1732
110 Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys
111                  80                  85                  90
113 tac tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag     1780
114 Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln
115                  95                  100                 105
117 acg cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc     1828
118 Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys
119      110                 115                 120
121 aac ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa     1876
122 Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu
123 125                 130                 135                 140
125 ttt gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg     1924
126 Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val
127                  145                 150                 155
129 atg gtg ctg cgc tgg agt gac ggc agt tat ctg gaa gat cag gat atg     1972
130 Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met
131                  160                 165                 170
133 tgg cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg     2020
134 Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro
135      175                 180                 185
137 act aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat     2068
138 Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp
139      190                 195                 200
141 ttc agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg     2116
142 Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu
143 205                 210                 215                 220
145 cgt gac tac cta cgg gta aca gtt tct tta tgg cag ggt gaa acg cag     2164
146 Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln
147                  225                 230                 235
149 gtc gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt     2212
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150 Val Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg
151           240              245              250
153 ggt ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg   2260
154 Gly Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro
155           255              260              265
157 aaa ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa   2308
158 Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu
159     270              275              280
161 ctg cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc   2356
162 Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val
163 285              290              295              300
165 ggt ttc cgc gag gtg cgg att gaa aat ggt ctg ctg ctg ctg aac ggc   2404
166 Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly
167           305              310              315
169 aag ccg ttg ctg att cga ggc gtt aac cgt cac gag cat cat cct ctg   2452
170 Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu
171     320              325              330
173 cat ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg   2500
174 His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu
175     335              340              345
177 atg aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac   2548
178 Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn
179     350              355              360
181 cat ccg ctg tgg tac acg ctg tgc gac cgc tac ggc ctg tat gtg gtg   2596
182 His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val
183 365              370              375              380
185 gat gaa gcc aat att gaa acc cac ggc atg gtg cca atg aat cgt ctg   2644
186 Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu
187           385              390              395
189 acc gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga   2692
190 Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg
191     400              405              410
193 atg gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg   2740
194 Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu
195     415              420              425
197 ggg aat gaa tca ggc cac ggc gct aat cac gac gcg ctg tat cgc tgg   2788
198 Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp
199     430              435              440
201 atc aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa ggc ggc gga   2836
202 Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly
203 445              450              455              460
205 gcc gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg   2884
206 Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val
207           465              470              475
209 gat gaa gac cag ccc ttc ccg gct gtg ccg aaa tgg tcc atc aaa aaa   2932
210 Asp Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys
211     480              485              490
213 tgg ctt tcg cta cct gga gag acg cgc ccg ctg atc ctt tgc gaa tac   2980
214 Trp Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr
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215          495                    500                      505
217 gcc cac gcg atg ggt aac agt ctt ggc ggt ttc gct aaa tac tgg cag    3028
218 Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln
219     510                        515                      520
221 gcg ttt cgt cag tat ccc cgt tta cag ggc ggc ttc gtc tgg gac tgg    3076
222 Ala Phe Arg Gln Tyr Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp
223 525                        530                        535          540
225 gtg gat cag tcg ctg att aaa tat gat gaa aac ggc aac ccg tgg tcg    3124
226 Val Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser
227             545                        550                      555
229 gct tac ggc ggt gat ttt ggc gat acg ccg aac gat cgc cag ttc tgt    3172
230 Ala Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys
231         560                        565                      570
233 atg aac ggt ctg gtc ttt gcc gac cgc acg ccg cat cca gcg ctg acg    3220
234 Met Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr
235         575                        580                      585
237 gaa gca aaa cac cag cag cag ttt ttc cag ttc cgt tta tcc ggg caa    3268
238 Glu Ala Lys His Gln Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln
239     590                        595                      600
241 acc atc gaa gtg acc agc gaa tac ctg ttc cgt cat agc gat aac gag    3316
242 Thr Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu
243 605                        610                        615          620
245 ctc ctg cac tgg atg gtg gcg ctg gat ggt aag ccg ctg gca agc ggt    3364
246 Leu Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly
247             625                        630                      635
249 gaa gtg cct ctg gat gtc gct cca caa ggt aaa cag ttg att gaa ctg    3412
250 Glu Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu
251         640                        645                      650
253 cct gaa cta ccg cag ccg gag agc gcc ggg caa ctc tgg ctc aca gta    3460
254 Pro Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val
255         655                        660                      665
257 cgc gta gtg caa ccg aac gcg acc gca tgg tca gaa gcc ggg cac atc    3508
258 Arg Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile
259 670                        675                        680
261 agc gcc tgg cag cag tgg cgt ctg gcg gaa aac ctc agt gtg acg ctc    3556
262 Ser Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu
263 685                        690                        695          700
265 ccc gcc gcg tcc cac gcc atc ccg cat ctg acc acc agc gaa atg gat    3604
266 Pro Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp
267             705                        710                      715
269 ttt tgc atc gag ctg ggt aat aag cgt tgg caa ttt aac cgc cag tca    3652
270 Phe Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser
271         720                        725                      730
273 ggc ttt ctt tca cag atg tgg att ggc gat aaa aaa caa ctg ctg acg    3700
274 Gly Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr
275         735                        740                      745
277 ccg ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc    3748
278 Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly
279     750                        755                      760
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281 gta agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg    3796
282 Val Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp
283 765                 770                 775                 780
285 aag gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg    3844
286 Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr
287                 785                 790                 795
289 gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg    3892
290 Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp
291                 800                 805                 810
293 cag cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att    3940
294 Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile
295                 815                 820                 825
297 gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc    3988
298 Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser
299     830                 835                 840
301 gat aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag    4036
302 Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln
303 845                 850                 855                 860
305 gta gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat    4084
306 Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr
307                 865                 870                 875
309 ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg    4132
310 Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu
311                 880                 885                 890
313 tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc    4180
314 Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg
315                 895                 900                 905
317 tgc ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac    4228
318 Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp
319     910                 915                 920
321 ttc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc    4276
322 Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr
323 925                 930                 935                 940
325 agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc    4324
326 Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile
327                 945                 950                 955
329 gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca    4372
330 Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser
331                 960                 965                 970
333 gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg    4420
334 Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu
335                 975                 980                 985
337 gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat    4468
338 Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His
339     990                 995                 1000
341 cat cat cat cat cac cgg taataatagg tagataagtg actgattaga           4516
342 His His His His His Arg
343 1005                 1010
345 tgcattgatc cctcgaccaa ttccggttat tttccaccat attgccgtct tttggcaatg  4576
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